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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:03:02; Search time 32017 Seconds (without alignments)

Title: US-10-049-743-1

Perfect score: 3868
Sequence: 1 gaattcggcacgacggccg.....ggtcttgggtacgagattc 3868
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 630880
Minimum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum DB seq length: 30

Post-processing: Minimum Match 100%
Listing first 45 summaries

GenEmbl:*

1: 9b_Da:*

2: 9b_btg:*

4: 9b_on:*

6: 9b_pat:*

7: 9b_pt:*

10: 9b_pt:*

10: 9b_pt:*

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12: 9b_pt:*

13: 9b_pt:*

14: 9b_vi:*

15: em_ba:*

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16: em_con:*

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23: em_tgi:*

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25: em_tgi:*

26: em_tgi:*

27: em_tgi:*

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29: em_tgi:*

29: em_tgi:*

20: em_tgi:*

Pred. No. is the number of results predicted by chance to have a

em_htgo_mus:*
em_htgo_other:*

em_htgo_hum:*

1 (bases 1 to 26) Chantry, D. H., Hoekstra, M.F. and Holtzman, D.A. Lipid kinase Patent: US 5858753-A 9 12-JAN-1999; Location/Qualifiers

REFERENCE AUTHORS TITLE JOURNAL FEATURES

Unknown. Unclassified.

Unknown.

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 1 AR028693/c LOCUS

PAT 29-SEP-1999

linear

DNA

Sequence 9 from patent US 5858753. AR028693.1 GI:5940666

ALIGNMENTS

AROBESOS Sequence
ARO28695 Sequence
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ARO28699 Sequence
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PAT 07-SEP-2000
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C Tantry/D.H., Hoekstra,M.F. and Holtzman,D.A.
Lipid kinase
AL Patent: US 5858753-A 12 12-JAN-1999;
Location/Qualifiers
1. .23
                                                                                                              1 (bases 1 to 25)
Chantry, D. H., Hoekstra, M.F. and Holtzman, D.A.
Lipid kinase
Patent: US 5985589-A 10 16-NOV-1999;
Location/Qualifiers
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Patent: 18, 5858753-A 11 12-JAN-1999;
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Sequence 10 from patent US 5985589.
AR086505
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Sequence 11 from patent US 5858753.
AR028695.1 GI:5940668
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Sequence 12 from patent US 5858753.
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1 (bases 1 to 26)
Chantry, D.H., Hoekstra, M.F. and Holtzman, D.A.
Lipid kinase
Patent: US 5985589-A 9 16-NOV-1999;
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Chantry, D. H., Hoekstra, M.F. and Holtzman, D.A.
Lipid kinase
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Sequence 10 from patent US 5858753.
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Sequence 9 from patent US 5985589.
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AR028694/c
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RESULT 4

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Chantry, D. H., Hoekstra, M.F. and Holtzman, D.A.
Lipid kinase
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( lasses 1 to 21)

Chantry, D.H., Hoekstra, M.F. and Holtzman, D.A.

Lipid kinase

Patent: US 5858753-A 7 12-JAN-1999;

Location/Qualifiers
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Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
Lipid kinase
Patent: US 5985589-A 14 16-NOV-1999;
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Best Local Similarity 100.0%; Pred. No. 8.8e+06;
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    Sequence 14 from patent US 5858753.
AR028698.1 GI:5940671
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AR086509
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Chantry, D. H., Hoekstra, M. F. and Holtzman, D. A.
Lipid kinase
Patent: US 5985589-A 12 16-NOV-1999;
Location/Qualifiers
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Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
Libid kinase
Patent: US 5985589-A 11 16-NOV-1999;
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1 Similarity 100.0%; Pred. No. 5.8e+06;
23; Conservative 0; Mismatches 0;
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6 c 10 g
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RESULT 8
AR086507/c
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ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

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JOURNAL

FEATURES

BASE COUNT

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RESULT 9 AR028698/c

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FEATURES TITLE

BASE COUNT

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RESULT 7 AR086506/c

LOCUS

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Job time : 32020 secs
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Chantry, D.H., Hockstra, M.F. and Holtzman, D.A.
Lipid kinase
Patent: US 5858753-A 8 12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.
1 (bases 1 to 21)
(Chantry, D.H., Hoekstra, M.F. and Holtzman, D.A.
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                                  Query Match 0.5%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 21; Conservative 0; Mismatches
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Sequence 16 from patent US 5858753.
AR028699 1GI:5940672
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                                                                                                                 Unclassified.

1 (bases 1 to 21)
Chantry, D.H., Hoekstra, M.F. and Holtzman, D.A.
Libid kinase
Patent: US 5985589-A 7 16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chantry, D. H., Hoekstra, M.F. and Holtzman, D.A. Libid kinase Patent: 18 5985589-A 8 16-NOV-1999; Location/Qualifiers
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Sequence 7 from patent US 5985589.
AR086502
AR086502.1 GI:10013268
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Sequence 8 from patent US 5985589.
AR086503
AR086503.1 GI:10013269
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES			Description	Phosphatidylinosit	PCR primer used to	Human PI 3-kinase-	Phosphatidylinosit	PCR primer used to	Human PI 3-kinase-	Phosphatidylinosit	Phosphatidylinosit	Probe used to isol
	æ		a	AAV31345	AAX15937	AAZ32887	AAV31346	AAX15938	AAZ32888	AAV31347	AAV31348	AAX15939
			DB	19	50	21	19	50	21	13	19	20
			Match Length DB	26	26	26	25	25	25	23	23	23
		Query	Match	0.7	0.7	0.7	9.0	9.0	9.0	9.0	9.0	9.0
			Score	26	26	26	25	25	25	23	23	23
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Probe used to isol Human PI 3-kinase-Human PI 3-kinase-Phosphatidylinosit PCR primer used to Human PI 3-kinase-Polymorphic fragme Polymorphic fragme Phosphatidylinosit Phosphatidylinosit Posphatidylinosit PCR primer used to PCR primer used t	TS a subunit RACE primer. lta; human; immune system; RACE; ss. Agent activity in immune system
AAX15940 AAZ32890 AAX32890 AAV31350 AAV31350 AAV31344 AAV31341 AAV31351 AAV31351 AAV31351 AAV31351 AAX15936 AAX15936 AAX15936 AAX15936 AAX15936 AAX15936 AAX15936 AAX13120 AAA13120 AAA13130	ALIGNMEN P110 delt p110 delt p11caen Da ltzman Da ltzman Da nase cata ng kinase
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                                                                          2 Antisense gene-specific oligonucleotide primers (see AAV31345 and AAV31346) respectively comprise a primary RACE primer and a nested RACE primer, and are based on the 5' end of M#928, a cDNA clone obtained from human macrophage cDNA by PCR amplification (see AAV31343-44). They were used to amplify 5' sequences of human phosphatidylinostiol 3-kinase (PI 3-kinase) pl10 delta catalytic subunit cDNA, using leucocyte cDNA as template. Amplified products were used as templates in a nested PCR and the reamplified products were then analysed using probes (see AAV31347-48) specific for pl10 partial clones #249 and M#928 to product a composite cDNA (AAV31340) sequence coding for human PI 3-kinase pl10 delta catalytic subinit (see AAW58570). This can be used to develop products for modulating and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primers AAX15937-38 were used to isolate cDNA encoding a catalytic subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase enzyme which is involved in PI3-Kinase mediated signalling in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase; p13-Kinase mediated signalling; immune system; phosphatidylinositol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19; Len.
7. 3.5e+04;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoekstra MF, Holtzman DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1500 GGGAACGCTGCCTCTACATGTGGCCC 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PI; kinase activity; PCR primer; ss.
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                                         Example 1; Page 11; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 GGGAACGCTGCCTCTACATGTGGCCC 1
  signalling and in carcinogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX15937 standard; DNA; 26 BP.
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96US-0777405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
hes 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                carcinogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ID AAX15937/C
XX AAX15937/C
XX AAX1593
XX Cataly;
XW PI3-Kii
XX Cataly;
XW PI3-Kii
XX Cataly;
XX Ca
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Lipid kinase; catalytic; subunit; pl10-delta; PI 3-kinase; phospharylation; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PRC; leukocyte activation; interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator; antagonist; agonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents human pl10-delta PCR primer #9, used in the generation of a full-length cDNA (AA232882) encoding a novel lipid kinase catalytic subunit, pl10-delta, related to phosphatidylinositol 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a membrane-localising p85 subunit and a catalytic pl10 subunit. These subunits both have isoforms, p85 has two isoforms (alpha and beta) which (alpha, beta and gamma) that vary in their ability to associate with p81 3-kinase phosphorylates PI and phosphorylated derivatives of PI at the 3' hydroxyl of the inositol ring with the primary product of PI 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5) triphosphate (PIP3). PI 3-kinase is activated by interaction with G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #9.
immune system. pl10-delta phosphorylates phosphatidylinositol (PI), and derivatives of it at the 3'-hydroxyl of the inositol ring). pl10-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (le blocking, inhibiting or stimulating) the binding between pl10-delta and its binding partner. pl10-delta may also be used in assays to identify modulators which inhibit or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying modulators of lipid kinase subunit pl10delta activity
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0
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 20; I
Pred. No. 3.5e+04;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1500 GGGAACGCTGCCTCTACATGTGGCCC 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 GGGAACGCTGCCTCTACATGTGGCCC 1
                                                                                                                                                                                                                                                                                                                                                              Ouery Match 0.7%; Sco
Best Local Similarity 100.0%; Pr
                                                                                                                                                                                                                                                            activate its kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ32887 standard; DNA; 26 BP
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25-NOV-1996;
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proteins and PI 3-kinase activation is believed to be involved in a apoptosis. The downstream targets of the phosphorylated lipids generated following PI 3-kinase activation have not been well characterised, although some isoforms of protein kinase C (PKC) are directly activated apperts of protein kinase C (PKC) are directly activated aspects of leukocyte activation, such as interleukin-2 (IL-2) production in T cells, and leukocyte signalling through G-protein coupled to receptors. pl10-delta, or nucleotides encoding it, may be used to identify modulators of pl10-delta and/or PI 3-kinase activity. These may be useful in the treatment of disorders associated with cell growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV31345) respectively comprise a primary RACE primer and a nested
AAV31346) respectively comprise a primary RACE primer and a nested
RACE primer, and are based on the 5' end of M#928, a cDNA clone
cobtained from human macrophage cDNA by PCR amplification (see
AAV31343-44). They were used to amplify 5' sequences of human
phosphatidylinostic) 3'kinase (PI 3'kinase) pl10 delta catalytic
subunit cDNA, using leucocyte cDNA as template. Amplified products
were used as templates in a nested PCR and the reamplified products
were then analysed using probes (see AAV31347-48) specific for pl10
celta. The specific 5' RACE PCR products were combined with
partial clones #249 and M#928 to produce a composite cDNA (AAV31340)
sequence coding for human PI 3'kinase pl10 delta catalytic subinit
(see AAW58570). This can be used to develop products for modulating
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New phosphatidylinositol 3-kinase catalytic subunit - used to develop products for modulating kinase activity in immune system signalling and in carcinogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphatidylinositol 3-kinase; p110 delta; human; immune system; carcinogenesis; diagnosis; PCR; primer; RACE; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphatidylinositol 3-kinase p110 delta subunit RACE primer.
                                                                                                                                                                                                                                       Length 26;
                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                           cell differentiation, apoptosis or immune activation.
                                                                                                                                                                                                                                  Query Match

0.7%; Score 26; DB 21; I
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                        Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                  1500 GGGAACGCTGCCTCTACATGTGGCCC 1525
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                                                                                                                                                                                                                                                                                                                    26 GGGAACGCTGCCTCTACATGTGGCCC 1
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AAV31346/C
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase; P13-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer used to amplify cDNA sequence encoding p110-delta.
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                                                                                                                                         Length 25;
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                                                                                                                                                                                             Indels
PI 3-kinase activity in immune system signalling and in carcinogenesis.
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Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                0.6%; Score 25; DB 19; 1
100.0%; Pred. No. 5.6e+04;
tive 0; Mismatches 0;
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                                                                                   Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                25 GGCGGACTGCCCCATTGCCTGGGCC 1
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ID AAX15938 standard; DNA; 25 BP.
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96US-0777405
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                                                                                                                                                                   Best Local Similarity 100.0 Matches 25; Conservative
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25-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                               Query Match
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Indels

.; 0

Mismatches

.; 0

Conservative

25;

Matches

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This sequence represents nument piro-tering a novel lipid finase catalytic subunit, pilo-delta, related to phosphatidylinositol and stanse (PI 3-Kinase). PI 3-Kinase is a heterodimer consisting of a mombrane-localising p85 subunit and a catalytic pilo subunit. These cate differentially expressed, and pilo has to date three isoforms are differentially expressed, and pilo has to date three isoforms (alpha, beta and gamma) that vary in their ability to associate with p85. PI 3-Kinase phosphorylates PI and phosphorylated derivatives of PI at the inositol ring with the primary product of PI 3-kinase phosphorylation being phosphatidylinositol (3, 4, 5) triphosphate (PIP3). PI 3-Kinase activation being phosphatidylinositol (3, 4, 5) triphosphate (PIP3). PI 3-Kinase including cell growth, differentiation and proptosis. The downstream targets of the phosphorylated lipids generated collowing PI 3-kinase activation have not been well characterised, although some isoforms of protein kinase (PKC) are directly activated by PIP3 in vitro. PI 3-kinase also given as interleukin-2 (IL-2) production aspects of leukocyte activation, such as interleukin-2 (IL-2) production aspects of leukocyte activation, such as interleukin-2 (IL-2) production aspects of leukocyte signalling through G-Protein coupled ceeptors. Pilo-delta, or nucleotides encoding it, may be used to cleentify modulators of pilo-delta and/or PI 3-kinase activity. These may come isoforms of pilo-delta and/or PI 3-kinase activity, interesting and proverse and percentants and percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipid kinase; catalytic; subunit; pil0-delta; pi 3-kinase; phosphorylation; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol (3, 4, 5) triphosphate; pris; activation; generalizar response; growth; differentiation; apoptosis; bhosphorylated lipid; protein kinase C; PRC; leukocyte activation; interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator; antagonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents human pl10-delta PCR primer #10, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying modulators of lipid kinase subunit pl10delta activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be useful in the treatment of disorders associated witcell differentiation, apoptosis or immune activation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chantry DH;
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25 GGGGACTGCCCATTGCCTGGGCC 1
                                                                                                                                                                   AA232888/C

AA232888 standard; DNA; 25 BP.
XX
XX
XX
AA232888;
XX
DY 09-FEB-2000 (first entry)
XX
Lipid kinase; catalytic; subut phosphatidylinositol 3-kinase, phosphatidylinositol 3-kinase, phosphatidylinositol 3-kinase, phosphatidylinositol 3-kinase, phosphatidylinositol 3-kinase, phosphatidylinositol 3-kinase, kW miagonist; agonist; treatment in interleukin.
XX
A miagonist; agonist; treatment kW miagonist; agonist; treatment in interleukins.
XX
Synthetic.
Synthetic.
Synthetic.
Synthetic.
AX
CS985589-A.
BP 16-NOV-1999; 97US-025951.
XX
CS985589-A.
BP 16-NOV-1999; 97US-0377871.
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CC 5-NOV-1999; 97US-025951.
XX
A 1COS-) ICCS CORP.
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A 16-NOV-1999; 97US-025951.
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A 1COS-) ICCS CORP.
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A 16-NOV-1999; 97US-0377871.
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A 16-NOV-1999; 97US-0377871.
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CC 6-JAN-1999; 97US-0377871.
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A 16-NOV-1999; 97US-0377871.
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A 16-NOV-1999; 97US-0377871.
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CC 7-NOV-1999; 97US-0377871.
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A 16-NOV-1999; 97US-0377871.
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A 16-NOV-1999; 97US-0377871.
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CC 7-NOS-012785/01.
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A 16-NOV-1999; 97US-0377871.
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A 16-NOV-1999; 97US-0377871.
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CC 7-NIS sequence represents human generation of a full-length of a full of a full-length of a spects of leukocyte activation of a full-length of a spects of leukocyte activation of a full-length of a spects of leukocyte activation of a full-length of the length of a full-length of a full-length of a full-length
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C; lU G, .

0.6%; Score 23; DB 19; Le
Pred, No. 1.4e+05;
Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;
                                                                          1149 CCCTGGAGCAGCGTTCCGCATC 1171
                      Query Match 0.6%; Scc
Best Local Similarity 100.0%; Pr
Matches 23; Conservative 0;
                                                                                                                                                                  BP.
                                                                                        23 CCCTGGAGCAGCCGTTCCGCATC
                                                                                                                                                                AAV31348 standard; DNA; 23
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                 12-0CT-1998
                                                                                                                                                                                         AAV31348;
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ID AAV3134
XX
AC AAV3134
XX
DT 12-OCT-
XX
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Length 25;

0.6%; Score 25; DB 21; 1 100.0%; Pred. No. 5.6e+04;

Query Match Best Local Similarity

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   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphatidylinositol 3-kinase; p110 delta; human; immune system; carcinogenesis; diagnosis; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphatidylinositol 3-kinase p110 delta subunit probe.
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                                                                       1459
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                                                               1435 GGCGGACTGCCCCATTGCCTGGGCC
                                                                                                              25 GGCGGACTGCCCCATTGCCTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US21655.
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ID AAV31347 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0777405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chantry DH, Hoekstra MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-322736/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09823760-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-NOV-1997;
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Homo sapiens. WO9823760-A1

Synthetic.

25-NOV-1997;

04-JUN-1998

25-NOV-1996;

Chantry DH,

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Catalytic subunit; pl10-delta; phosphatidylinositol 3-kinase; pl3-kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which
                                                                                                                                                                                                                                                                                                                         subunit (pilo-delta), derived from a Phosphatidylinositol 3-Kinase enzyme which is involved in Pi3-Kinase mediated signalling in the immune system. pilo-delta phosphorylates phosphatidylinositol [PI], and derivatives of it at the 3'-hydroxyl of the inositol ring). pilo-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (ie blocking, inhibiting or stimulating) the binding between pilo-delta and its binding pertner. pilo-delta may also be used in assays to identify modulators which inhibit or activate its kinase activity.
                                                                                                                                                                    Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and
                                                                                                                                                                                                                                                                                                             Probes AAX15939-40 were used to isolate cDNA encoding a catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 23; DB 20; I
100.0%; Pred. No. 1.4e+05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;
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                                                                                                  Holtzman DA;
                                                                                                                                                                                                                                                                          Example 1; Columns 7; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1149 CCCTGGAGCAGCCGTTCCGCATC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 CCTGGAGCAGCCGTTCCGCATC 1
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960S-0777405.
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97US-0977871.
96US-0777405.
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                                                                                                  Hoekstra MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
hes 23; Conservative
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                                                                                                                                     WPI; 1999-214067/18.
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                                                           (ICOS-) ICOS CORP.
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25-NOV-1996;
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  25-NOV-1997;
25-NOV-1996;
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                                                                                                    Chantry DH,
                                                                                                                                                                                                                                         co-factors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catalytic subunit; pl10-delta; phosphatidylinositol 3-kinase; pl3-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  New phosphatidylinositol 3-kinase catalytic subunit - used to develop products for modulating kinase activity in immune system signalling and in carcinogenesis
                                             Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
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0.6%; Score 23; DB 19; Length zo,
nnn.0%; Pred. No. 1.4e+05;
nnn.0%; Pred. No. 1.4e+05;
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      Phosphatidylinositol 3-kinase p110 delta subunit probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
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                                                                 carcinogenesis; diagnosis; probe; ss.
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AAX15939/c
ID AAX15939 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                                                              Hoekstra MF,
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Best Local Similarity 100.
Matches 23; Conservative
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JS5882910-A 16-MAR-1999

Synthetic.

AAX15939;

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Gaps

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membrane-localising p85 subunit and a catalytic p110 subunit. These subunits both have isoforms; p85 has two isoforms (alpha and beta) which care differentially expressed, and p110 has to date three isoforms (alpha, beta and gamma) that vary in their ability to associate with p85. P13 *Athase phosphorylates P1 and phosphorylated derivatives of P1 at the 3' hydroxyl of the inositol ring with the primary product of P1 3. *Athase phosphorylation being phosphatidylinositol (3, 4, 5) triphosphate (PPP). P1 3.*Athase is activated by interaction with G proteins and P1 3.*Athase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and a proteins and P1 3.*Athase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and approteis. The downstream targets of the phosphorylated lipids generated following P1 3.*Athase activation have not been well characterised, although some isoforms of protein kinase C (PKC) are directly activated by print in vitro. P1 3.*Athase also appears to be involved in certain aspects of leukocyte signalling through G-protein coupled coupled to cells, and leukocyte signalling through G-protein coupled coupled the cells, and leukocyte signalling through G-protein coupled cells and cells, and the transment of disorders associated with cell growth, associated with cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipid kinase; catalytic; subunit; pl10-delta; pl 3-kinase; phosphorylation; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol (3, 4, 5) triphosphate; plP3; activation; G protein; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PRC; leukocyte activation; interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator; antagonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dentifying modulators of lipid kinase subunit pl10delta activity -
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100.0%; Pred. No. 1.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Preq. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1149 CCCTGGAGCAGCGGTTCCGCATC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 CCTGGAGCAGCGGTTCCGCATC 1
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AAZ32890 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dipid kinase; catalytic; subunit; p110-delta; PI 3-kinase; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PRC; leukocyte activation; interleukin 2: IL-2; production; T cell; leukocyte signalling; modulator; antagonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents human pll0-delta PCR primer #11, used in the generation of a full-length cDNA (AAZ32882) encoding a novel lipid kinase catalytic subunit, pll0-delta, related to phosphatidylinositol 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #11.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                             Probes AAX15939-40 were used to isolate cDNA encoding a catalytic subunit (pl10-delta), derived from a Phosphatidylinositol 3-kinase enzyme which is involved in p13-Kinase mediated signalling in the immune system. pl10-delta phosphorylates phosphatidylinositol (PI), p110-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, so an antibodies (using standard techniques) which may be used, for example, to modulate (ie blocking, inhibiting or stimulating) the almoing between p110-delta and its binding partner. p110-delta may activate its kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying modulators of lipid kinase subunit p110delta activity
    modulate the enzymes kinase activity or binding to substrates and
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                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 23; DB 20; Length 23
100.0%; Pred. No. 1.4e+05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
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                                                           Example 1; Columns 7; 22pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1132 CTCTGTGTCCCTGTGGTCCCTGG 1154
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960S-0777405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Les 23; Conservative
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25-NOV-1996;
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constraint of a full-length CDNA (AA212882) encoding a novel lipid kinase catalytic subunit, pl10-delta, related to phosphatidylinositol 3 kinase (pr 13 kinase). Pl 3 kinase is a heterodimer consisting of a membrane-localising p85 subunit and a catalytic pl10 subunit. These subunits both have isoforms; p85 has two isoforms (alpha and beta) which are differentially expressed, and p110 has to date three isoforms. C alpha, beta and gamma) that vary in their ability to associate with p85. Pl 3 kinase phosphorylation ring with the primary product of P1 a kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5) triphosphate (PIP3). Pl 3 kinase is activated by interaction with G proteins and P1 3 kinase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and apoptosis. The downstream targets of the phosphorylated lipids generated following P1 3 kinase activation have not been well characterised, although some isoforms of protein kinase C (PKC) are directly activated by PIP3 in vitro. P1 3 kinase also appears to be involved in certain aspects of leukocyte activation, such as interleukin-2 (IL-2) production aspects of leukocyte activation, such as interleukin-2 (IL-2) production receptors. P100 delta, or nucleotides encoding it, may be used to cell differentiation, anothors activation and setting mediators of p110-delta and/or P1 3 kinase activity. These may be all differentiation, anothors activation and intermed and activity may be used to receptors.
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sequence represents human pl10-delta PCR primer #12, used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphatidylinositol 3-kinase; p110 delta; human; immune system; carcinogenesis; diagnosis; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell differentiation, apoptosis or immune activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 21; I; Pred. No. 1.4e+05; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1132 CTCTGTGTCCCTGTGGTCCCTGG 1154
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Best Local Similarity 100.0
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AAV31350/c
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catalytic subunit; pl10-delta; phosphatidylinositol 3-kinase; PI3-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; PCR primer; ss.
amplification of 5'RACE PCR products (see AAV31345-46) of human leukocyte cDNA. The 5' primer includes a 5' BamHI site and sequences that code for a FLAG peptide (see AAW88571) which is product was combined with restriction fragments of partial clones #290 and ##928 to produce a full-length cDNA (see AAV31347) for the ploop and ##928 to produce a full-length cDNA (see AAV31347) for the phosphatidylinositol 3-kinase (PI 3-kinase). This was incorporated into expression vector pcDNA3, and FLAG-tagged pl10 delta was expressed in transfected COS cells. pl10 delta can be used to system signalling and in carcinogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel catalytic subunits derived from phosphatidylinositol 3-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer used to amplify cDNA sequence encoding p110-delta.
                                                                                                                                                                                                                                                                     Length 22;
                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                0.6%; Score 22; DB 19; I
                                                                                                                                                                                                                                    Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                         Pred. No. 2.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                          1501 GGAACGCTGCCTCTACATGTGG 1522
                                                                                                                                                                                                                                                                                                                                                              22 GGAACGCTGCCTCTACATGTGG 1
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96US-0777405.
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                                                                                                                                                                                                                                                                                                         22; Conservative
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                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                       Query Match
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AAX15942/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipid kinase; catalytic; subunit; pll0-delta; pl 3-kinase; phosphorylation; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol (3, 4, 5) triphosphate; plPB; activation; G protein; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PKC; leukocyte activation; interleukin-2; ll-2; production; T cell: leukocyte signalling; modulator; antagonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #14.
                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                            ;
                                                                                                                                      Length 22;
                                                                                                                                                                                                        Indels
                                                                                                                                   0.6%; Score 22; DB 20; I
100.0%; Pred. No. 2.2e+05;
vative 0; Mismatches 0;
                                                                     Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                             1501 GGAACGCTGCCTCTACATGTGG 1522
                                                                                                                                                                                                                                                                                                                     22 GGAACGCTGCCTCTACATGTGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             892/c
AAZ32892 standard; DNA; 22 BP.
activate its kinase activity.
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                                                                                                                                                                                                            22; Conservative
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                                                                                                                                                                       Best Local Similarity
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25-NOV-1996;
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                                                                                                                                          Query Match
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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AAZ3289372
AAZ3280372
AAZ3280372
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in T cells, and leukocyte signalling through G-protein coupled receptors. pll0-delta, or nucleotides encoding it, may be used to identify modulators of pll0-delta and/or pr 3-kinase activity. These may be useful in the treatment of disorders associated with cell growth, cell differentiation, apoptosis or immune activation.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                          ;
0
                                                                                                                                                                              Length 22
                                                                                                                                                                                                                        Indels
                                                                                                                                   C; 6 G; ....
0.6%; Score 22; DB 21; Le
Pred. No. 2.2e+05;
0;
                                                                                                                                   Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 3, 2003, 20:12:24
Job time: 741 secs
                                                                                                                                                                                                                                                                 1501 GGAACGCTGCCTCTACATGTGG 1522
                                                                                                                                                                                                                                                                                               GGAACGCTGCCTCTACATGTGG 1
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                                                                                                                                                                                            Best Local Similaricy
                                                                                                                                                                              Query Match
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Run on:

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Gaps
                    Sequence 11, Sequence 12, Sequence 13, Sequence 15, Sequence 15, Sequence 16, Sequence 16, Sequence 20, Sequence 21, Sequence 22, Sequence 23, Sequence 23, Sequence 24, Sequence 25, Sequence 27, Seque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 58587538nd, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
US-09-357-070-10

US-09-357-070-11

US-09-357-070-12

US-09-357-070-14

US-09-357-070-14

US-09-357-070-15

US-09-357-070-16

US-09-357-070-18

US-09-357-070-19

US-09-357-070-20

US-09-357-070-21

US-09-357-070-22

US-09-357-070-25
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; Patent No. 5858753
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGH: 26 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.77
Best Local Similarity 100.
Matches 26; Conservative
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  TOPOLOGY: linear MOLECULE TYPE: CDNA
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      US-08-777-405A-9/C
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8786.857 Million cell updates/sec
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                                                                                                                                                                                                                                                                                       1 gaattcggcacgagcggccg.....ggtcttgggtacgagaattc 3868
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Sequence 9
Sequence 1
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Sequence 3
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Sequence
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                                                                                                                                                           March 3, 2003, 19:58:31; Search time 135 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                             GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-977-871A-9

US-08-977-871A-10

US-08-977-871A-10

US-08-977-871A-11

US-08-977-405A-11

US-08-977-405A-11

US-08-977-871A-11

US-08-977-871A-11

US-08-977-871A-11

US-08-977-871A-11

US-09-225-951-11

US-08-977-871A-14

US-08-977-871A-14

US-08-977-871A-14

US-08-977-871A-16

US-08-977-871A-16
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US-09-357-070-8
US-09-357-070-9
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    nucleic search, using sw model

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                                                                                                                                                                                                                                           US-10-049-743-1
3868
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 30
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Minimum DB Maximum DB

Database

Searched:

Sequence:

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us-10-049-743-1.1im30.rni

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Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-777-405A-10/C
Sequence 10, Application US/08777405A
Fatent No. 5858753
CENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hockstra, Marl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.7%; Score 26; DB 2; Le Best Local Similarity 100.0%; Pred. No. 2.4e+03; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                  SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/225,951
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGBNT INFORMATION:
NAME: No. 598589and, Greta E.
REGISTRATION NUMBER: 35,302
REBERRENCE/POCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-630
TELEPRA: (312) 474-0448
TELERA: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: NO. 588973and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6448
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1500 GGGAACGCTGCCTCTACATGTGGCCC 1525
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: CDNA
US-09-225-951-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Sear CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                              E: Marshall O'Toole Gerstein Murray & Borun
6300 Sears Tower/233 South Wacker Drive
                                                                   GS-08-977-871A-9/C

Sequence 9, Application US/08977871A

Parent No. 5882910

GENERAL INFORMATION:

APPLICANT: Chantry, David

APPLICANT: Hockstra, Merl F.

APPLICANT: Hockstra, Merl F.

APPLICANT: Holtzman, Douglas A

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall O'Toole Gerstein Murray & BC

STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 66666
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
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Patent No. 598589
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hotextra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION:
NUMBER OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION ...
RILING DATE:
RILING DATE:
NAME: No. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REPERROCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPAK: (312) 474-6448
TELEFAK: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEGURACE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

0.7%; Score 26; DB
Best Local Similarity 100.0%; Pred. No. 2.4
Matches 26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: CDNA
US-08-977-871A-9
                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-225-951-9/c
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E: Marshall O'Toole Gerstein Murray & Borun
6300 Sears Tower/233 South Wacker Drive
                               APPLICANT: Chantry, David
APPLICANT: Chantry, David
APPLICANT: Hockstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall O'Toole Gerstein Murray & Borur
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Chantry, David
APPLICANT: Hockstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5888753e1 Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 25; DB 2;
illarity 100.0%; Pred. No. 4e+03;
Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27866/33441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08777405A Patent No. 5858753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5985589and, Greta E.
REGISTRATION NUMBER: 35,302
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELES: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear;
; MOLECULE TYPE: CDNA
US-09-225-951-10
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Matches 25; Conserva
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
                          GENERAL INFORMATION:
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US-08-777-405A-11/c
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                                                                                                                                          Length 25;
                                                                                                                                     Query Match 0.6%; Score 25; DB 2; Length 25; Best Local Similarity 100.0%; Pred. No. 4e+03; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chantry, David
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5882910el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Bo
STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.6%; Score 25; DB 2; Best Local Similarity 100.0%; Pred. No. 4e+03; Matches 25; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: NO. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELERX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                1435 GGCGGACTGCCCCATTGCCTGGGCC 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1435 GGCGGACTGCCCCATTGCCTGGGCC 1459
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Sequence 10, Application US/08977871A
Patent No. 5882910
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/777,405
FILING DATE:
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; Sequence 10, Application US/09225951
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STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                           ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-777-405A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: CDNA
US-08-977-871A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Length 25; 0; Indels

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          Indels
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APPLICANT: Hockstra, Merl F.
APPLICANT: Holzman, Douglas A
TITLE OF INFUNION: No. 5882910el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATSHAll O'TOOLE GETSTEIN MULTAY & BOTUN
STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
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Patent No. 5882910
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5882910e1 Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.6%; Score 23; DB 2; Best Local Similarity 100.0%; Pred. No. 1.1e+0. Matches 23; Conservative 0; Mismatches
        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: No. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPRICE: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    US-08-977-871A-11/c
; Sequence 11, Application US/08977871A
Patent No. 5882910
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
                                               1132 CTCTGTGTCCCTGTGGTCCCTGG 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1149 CCCTGGAGCAGCCGTTCCGCATC 1171
                                                                       23 CTCTGTGTCCCTGTGGTCCCTGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-977-871A-11
        23;
        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun STREET: 6300 Sears Tower/233 South Wacker Drive CITY: Chicago CTATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 23; DB 2; Lv Best Local Similarity 100.0%; Pred. No. 1.1e+04; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 2; LA
Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                       REFERENCE/DOCKET NUMBER: 27866/33441 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27866/33441
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
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; Sequence 12, Application US/08777405A
; Patent No. 5858753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DALL.

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
NAME: No. 5858753and, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1149 CCCTGGAGCAGCCGTTCCGCATC 1171
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TELERAX: 25-3856
INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENOTH: 23 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                          TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 CCCTGGAGCAGCCGTTCCGCATC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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100.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5: Marshall O'Toole Gerstein Murray & Borun 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/225,951
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100.0%; Pred. No. 1.1e+04;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27866/33441
                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
US-09-225-951-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: other nucleic acid US-09-225-951-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09225951; Patent No. 5985589; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           1149 CCCTGGAGCAGCGGTTCCGCATC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: No. 5985589and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1132 CTCTGTGTCCCTGTGGTCCCTGG 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 CTCTGTGTCCCTGTGGTCCCTGG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 23; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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Matches
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COUNTRY: USA
    S: Marshall O'Toole Gerstein Murray & Borun 6300 Sears Tower/233 South Wacker Drive
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 23; Conservative 0; Mismatches 0;
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APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: No. 5882010and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEXX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
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RATIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
FILING DATE:
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NAME: No. 5985589and, Greta E.
REGISTRATION NUMBER: 35,302
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MEDIUM TYPE: Floppy disk
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EDNESS: single
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                           CITY: Chicago
STATE: Illinois
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US-09-225-951-11/C
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      ADDRESSEE:
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                                                                               COUNTRY:
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0.6%; Score 22;
100.0%; Pred. No.
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NAME: No. 5985589and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
FILING DATE:
ATTORENY ADENTION:
NAME: No. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 27866/33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLGGY: linear MOLECULE TYPE: other nucleic acid US-08-977-871A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1501 GGAACGCTGCCTCTACATGTGG 1522
IBM PC compatible
                                                                                                                                                                                                                                                                                                       TELEPHONE: (312) 474-6300
TELERAX: (312) 474-6448
TELERX: 25-3856
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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(312) 474-0448
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TELEFA: 25-3856
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
Matches 22; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-977-871A-14/C
; Sequence 14, Application US/08977871A
; Patent No. 5882910;
; Patent No. The Chantry, David
; APPLICANT: Chantry, David
; APPLICANT: Hockstra, Merl F
; APPLICANT: Hockstra, Merl F
; APPLICANT: Hockstra, David
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
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                                                                                                                                 APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTIONS: 10. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; I
. 1.8e+04;
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100.0%; Pred. No. 1.8
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
                                             US-08-777-405A-14/c
; Sequence 14, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: other nucleic acid US-08-777-405A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-8856
INFORMATION FOR SO ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-09-225-951-14/C

i Sequence 14, Application US/09225951

i Patent No. 5985589

i GENERAL INFORMATION:

APPLICANT: Chantry, David

APPLICANT: Holtzman, Douglas A

TITLE OF INVENTION:

NOWBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun

STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 22;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SALEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-09-225-951-14

Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1501 GGAACGCTCCTTACATGTGG 1522

Qy 1501 GGAACGCTCCTTACATGTGG 152

Db 22 GGAACGCTCCTTACATGTGG 1

Search completed: March 4, 2003, 06:27:43
Job time : 136 secs
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Sequence 1, Appli
Sequence 379, Ap
Sequence 3780, Ap
Sequence 3780, Appl
Sequence 10, Appl
Sequence 16, Appl
Sequence 176, Appl
Sequence 3895, Ap
Sequence 3895, Ap
Sequence 4394, Ap
Sequence 4394, Ap
Sequence 12035, Ap
                                                                                      (without alignments)
2338.022 Million cell updates/sec
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                                                                          March 3, 2003, 20:00:22 ; Search time 1105 Seconds
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// Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
// Cgn2_6/ptodata/2/pubpna/NSO6_PUBCOMB.seq:*
// Cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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// Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-866-108-3799

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10S-09-866-108-3895

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10S-09-866-108-1394

10S-09-866-108-12894

10S-09-866-108-12899

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Maximum Match 100%
Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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3868
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Match Length
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length: 30
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65:
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17.6
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Maximum DB seq
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117
117
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Perfect so
Seguence:
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Sequence 12944, A Sequence 12985, A Sequence 13772, A Sequence 19, Appl Sequence 45, Appl Sequence 46, Appl Sequence 3896, Ap Sequence 3898, Ap Sequence 3899, Ap Sequence 2, Appl Sequence 2, Appl Sequence 19, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 3760, Ap Sequence 3760, Ap Sequence 3760, Ap Sequence 3761, Appl Sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ARABIRA, MASAOMI
APPLICANT: FUNCARA, CHIKAFUSA
TITLE OF INVENTION: METHOD FOR PREPARING TEMPLATE DNA FROM PROCESSED
TITLE OF INVENTION: WEGETABLE FOOD, WHICH IS FEASIBLE FOR AMPLIFICATION OF
TITLE OF INVENTION: DNA REGION BY PCR METHOD
FILE REFERENCE: 8361-0011-0
CURRENT APPLICATION NUMBER: U5/09/494,438
CURRENT APPLICATION NUMBER: U5/09/494,438
PRIOR FILING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PALENTIN VET: 2.1
SOFTWARE: PALENTIN VET: 2.1
LENGTH: 30
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Patent No. US20020127653A1
GENERAL INFORMATION:
ROPELTCANT: SOPET, DANIEL R.
RUBEN, STEVEN M.
TITLE OF INVENTION: HEMATOPOIETIC SIGNALING FACTOR
0.5-09-866-108-12944

0.5-09-866-108-13772

0.5-09-866-108-14859

0.5-09-729-6588-45

0.5-09-729-6588-45

0.5-09-729-6588-45

0.5-09-729-6588-45

0.5-09-866-108-3896

0.5-09-866-108-3898

0.5-09-866-108-3899

0.5-09-866-108-3899

0.5-09-866-108-3899

0.5-09-866-108-3899

0.5-09-866-108-3899

0.5-09-866-108-3899

0.5-09-866-108-3899

0.5-09-866-108-3899

0.5-09-866-108-3899

0.5-09-866-108-3900

10.5-09-852-000-5

10.05-09-852-000-5

10.05-09-756-095-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.5%; Score 20; DB 10; L. Best Local Similarity 82.1%; Pred. No. 8.3e+04; Matches 23; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                  US-09-866-108-3760
US-09-866-108-3761
US-09-866-108-3762
US-09-866-108-3943
US-09-866-108-3944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
        US-09-996-606-4/C
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        FEATURE
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Query Match 0.5%; Score 17.6; DB 10; Best Local Similarity 83.3%; Pred. No. 2.8e+05; Matches 20; Conservative 0; Mismatches 4;
                                               PRIOR AFFILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00065
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/284,687
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR PLILING DATE: 2001-01-02-05
NUMBER OF SEQ ID NOS: 15752
SSEQ ID NO 3779
FEBRICH NO 3779
FEBRICH NO 3779
FEBRICH NO 3779
       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2322 CCCAGACCAAGGAGCTGATGCACT 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CCCAGGCCAAGGAACTGTGGCACT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108-3779
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US-09-866-108-3780
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APPLICANT: 0U, Yizhong
APPLICANT: 0U, Yizhong
APPLICANT: DI, Yongsang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: SHANNON, Mark
ITILE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/236,56
PRIOR FILING DATE: 2000-05-25
PRIOR PLILOR DATE: 2000-00-47
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PRIOR PLILNG DATE: 2001-00-04
PRIOR PLILNG DATE: 2001-03-30
PRIOR PLILNG DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-01-03-30
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NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.5%; Score 18.6; DB 10; Length 29; Best Local Similarity 84.0%; Pred. No. 1.7e+05; Matches 21; Conservative 0; Mismatches 4; Indels (
                                                                                                              COMPUTER: DC
COUNTRY: US
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,606
FILING DATE: 30-No. US20020127653A1-2001
CLASSIFICATION NUMBER: US/09/996,606
FILING DATE: 30-No. US20020127653A1-2001
CLASSIFICATION NUMBER: US/09/908,490
FILING DATE: 4UNKnown>
RINGS STEFEE, ERIC K
RESISTRATION NUMBER: 36,688
REFERRENCE/DOCKEY NUMBER: 1488.0600001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-996-606-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3356 AGAGGAGGCGGCTGCGGGTCGTGGG 3380
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STRANDEDNESS: single
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Gaps

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Length 25; Indels

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Seguence 16, Application US/09804717A

Sequence 16, Application US/09804717A

Patent No. US20020164311A1

GENERAL INFORMATION:

APPLICANT: Strom, Tevia

APPLICANT: Libermann, Towia

TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION OF GRAFT REJECTION

FILE REFERENCE: 01948-051003

CURRENT APPLICATION NUMBER: US/09/804,717A

CURRENT FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1993-03-01

PRIOR FILING DATE: 1993-03-01

PRIOR FILING DATE: 1993-03-01

PRIOR FILING DATE: 1992-02-28

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 16

LENGTH: 22
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APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT APPLICATION NUMBER: 09/050,739
PRIOR PELICATION NUMBER: 0376/97
PRIOR PELICATION NUMBER: 1937-04.02
PRIOR FILING DATE: 1997-04.02
PRIOR FILING DATE: 1997-04.02
PRIOR FILING DATE: 1997-04.02
PRIOR FILING DATE: 1997-04.18
PRIOR PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 17.4; DB 10; Best Local Similarity 77.8%; Pred. No. 3.4e+05; Matches 21; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3268 TGAGAGCTGGAAAACCAAAGTGAACTG 3294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TGAGATCTAGAATGCCACAGGGAACTG 28
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Matches 19; Conservative
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ORGANISM: Homo sapiens
US-09-804-717A-16
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US-09-866-108-3764
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Sequence 20, Application US/09894633A

Patent No. US20020124285A1

GENERAL INFORMATION:
APPLICANT: Conner, Timothy

APPLICANT: Dubois, Patrice
APPLICANT: Malven, Marianne
APPLICANT: Malven, Marianne
APPLICANT: Malven, James
TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSI
FILE REFERENCE: 38-21(15856)B

CURRENT APPLICATION NUMBER: 06/214,357

FILE REFERENCE: 2000-06-28

PRIOR APPLICATION NUMBER: 60/214,357

PRIOR PPLICATION NUMBER: 09/894,633

PRIOR PPLICATION NUMBER: 2000-06-28

NUMBER OF SEQ ID NOS: 111

SEQ ID NO 20

SEQ ID NO 20

LENGTH: 28
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LOCATION: (1)..(28)
FORTH INFORMATION: synthetic primer sequence
US-09-894-6338-20
                    PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SEQ ID NO 3780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1587 ACACGGATAGCGCCGCTGCCTGCTCA 1613
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Patent No. US2002004335A1
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OFTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2322 CCCAGACCAAGGAGCTGATGCACT 2345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 83.3
Matches 20; Conservative
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US-09-866-108-3780
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US-09-894-633A-20/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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APPLICANT: GU, YIZHONG
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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80.0%; Pred. No. 3.9e+05;
tive 0; Mismatches 5
                                                   FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR PILING DATE: 2000-05-26

PRIOR PELICATION NUMBER: GB 24263.6

PRIOR PELING DATE: 2000-010-04

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING D
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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Patent No. US20020048800A1
GENERAL INFORMATION:
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Best Local Similarity 80.uv
Post Local Similarity
Conservative
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US-09-866-108-3778
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                                                                                                                                           APPLICANT: J1, Yonggang
APPLICANT: J1, Yonggang
APPLICANT: BENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
TILLE OF INVERTION WOBSEL: 2001-05-25
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PLIANG DATE: 2001-01-30
PRIOR PLIANG DATE: 2001-01-30
PRIOR PLIANG DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PRILNG DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 3764
LENGTH: 25
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PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
Sequence 3764, Application US/09866108
Patent No. US20020048800A1
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Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3367 CTGCGGGTCGTGGGGACCAAGCACA 3391
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: JI, Yongdang
: PENN, Sharron G
: HANZEL, David K.
: RANK, David R.
: CHEN, Wensheng
SHANNON, Mark
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ORGANISM: Homo sapiens
                                                                                                                       : GU, Yizhong
                                                                                   GENERAL INFORMATION:
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APPLICANT:
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Matches
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Gaps

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APPLICANT: CHEN, WALES
TITLE OF INVENTION: MACSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE REFERENCE: ABOMICA-7
CURRENT APPLICATION UNMERR: US/09/866,108
CURRENT FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-01-30
PRIOR PLING DATE: 2001-01-30
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80.0%; Pred. No. 3.9e+05;
tive 0; Mismatches 5; Indels
                                  PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: ADOMICA SEQUENCE LISTING Engine
SOFTWARE: 255
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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CORGANISM: Homo sapiens
US-09-866-108-3945
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Best Local Similarity
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US-09-866-108-4394
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US-09-866-108-3945
Sequence 3945, Application US/09866108
APPLICANT: US COMPANY DAVIG K.
APPLICANT: ENANK, DAVIG K.
APPLICANT: SHANNON, MAIK
STALICANT: SHANNON, MAIK
TITLE OF INVENTION: WOOSTH-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT PILLING DATE: 2001-05-25
PRIOR FILLING DATE: 2000-01-05-26
PRIOR FILLING DATE: 2000-01-00-04
PRIOR PLILING DATE: 2000-01-03
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
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   PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLILNG DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-02-05
NUMBER OF SECION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SECION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SECION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SECION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SECION NUMBER: US 60/266,860
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LENGTH: 25
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US-09-866-108-3895
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APPLICANT: RANK, DAVIG R.
APPLICANT: RANK, DAVIG R.
APPLICANT: GENE WARSHENG
APPLICANT: GENE WARSHENG
APPLICANT: GENE WARSHENG
APPLICANT: GENE WARSHENG
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEDMICA-7
CURRENT APPLICANTON NUMBER: US 60/207,456
PRIOR FILING DATE: 2001-05-26
PRIOR PELING DATE: 2000-10-6-25
PRIOR FILING DATE: 2000-10-6-26
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR PELING DATE: 2001-01-30
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                                                                                Length 25;
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80.0%; Pred. No. 3.9e+05;
iive 0; Mismatches 5;
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80.0%; Pred. No. 3.9e+05;
tive 0; Mismatches 5;
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                                                                                                                                                                                                                   654 GCCGGCAGCTGGGCTGGGAGGC 678
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                                                                                Query Match 0.4%
Best Local Similarity 80.0%
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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SOFTWARE: Acomica Sec
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US-09-866-108-12035
              US-09-866-108-4395
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APPLICANT:
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APPLICANY: RANK, David K.

APPLICANY: RANK, David K.

APPLICANY: SHANNON, MARK

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: MYDER: US/09/866,108

CURRENT PELIAGE DATE: 2001-05-25

PRIOR PELIAGE APPLICATION NUMBER: US 60/207,456

PRIOR PELIAGE DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR PELIAGE APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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80.0%; Pred. No. 3.9e+05;
iive 0; Mismatches 5;
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NUMBER OF SEQ ID NOS: 15752
SOFWARE: Aeomica Sequence Listing Engine
SO ID NO 4395
LEWGTH: 25
TYPE: DNA
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 4394
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEADLIA TO SEQUENCE 4195

Sequence 4195, Application US/09866108

Fatent No. US20020048800A1

GENERAL INFORMATION:
APPLICANT: GU, Yizhong

APPLICANT: JT, Yonggang

APPLICANT: PENN, Sharron

APPLICANT: HARZEL, DANIG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  653 CGCCGCCAGCAGCTGGGCTGGGAGG 677
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Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108-4394
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Gaps

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1. Sequence 12894, Application US/09866108
1. Sequence 12894, Application US/09866108
1. GENERAL INFORMATION:
1. RAPLICART: GU, YIZhong
1. APPLICART: GU, YIZhong
1. APPLICART: GU, YIZhong
1. APPLICART: HANKEL, David R.
1. APPLICART: HANKEL, David R.
1. APPLICART: SHANNON, WARK
1. TITLE REPRENENCE: ABOUTON: JOIN 105-25
1. FRIOR PRILING DATE: 2001-05-25
1. FRIOR PELLING DATE: 2001-05-25
1. FRIOR PELLING DATE: 2001-01-30
1. FRIOR PERLING DATE: 2001-01-30
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; ORGANISM: Homo sapiens
US-09-866-108-12894
US-09-866-108-12894
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Search completed: March 4, 2003, 06:46:21 Job time: 1106 secs

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AA973948 oq12d02.8
BM39817 5009-0-46
AZ404206 1M0172120
AZ789420 2M0037JJ1
AZ840149 2M0136M06
AA553755 Om89D03.8
BM398127 5009-0-41
AZ34274 1M0076C04
AZ601864 1M0420P16
AA766400 ca36e03.8
AL479776 T. brucel
AZ371129 1M0122M02
AZ371129 1M0179123
AZ4786739 1M0179123
AZ4786739 1M0179123
AZ4786740 1M0080124
AZ502451 1M0341D17
AU269375 AU269375
D45817 HUMGS03036
AV852654 AN852654
H41620 yco90909 r1
BH810436 SALK_0495
AZ36815 1M0010820
AZ36819 1M0010820
AZ36819 1M0013622
AZ375573 2M0016809
BM401118 5009-0-82
AZ37691 1M0029502
AZ368069 1M0010N09
AZ368069 1M0013032
AZ46582 1M00295018
AZ46322508 2M0027807
AZ822508 2M0027807
AZ822508 2M0027807
AZ62456 5x422666.x
A1652245 5x422666.x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other ESTs: ybl3b04.sl
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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AZ371129
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BH861248 SALK_0678
AA479681 1M0300G02
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13255.214 Million cell updates/sec
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                                                                                              March 3, 2003, 19:51:57; Search time 4726 Seconds
                                                                                                                                                                                                                                                                 30108
                  GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
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Listing first 45 summaries
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Score

Result М В 16.8 16.8

Post-processing:

Database

Scoring table:

Searched:

Perfect score:

Sequence:

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Run on:

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Gaps

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Indels

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SALK_067873 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_067873, DNA sequence.
BH861248
BH861248.1 GI:22096574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Stratagene Chick Embryo Lambda cDNA Library (* 937405)"
                                                                                                                                                                                                       AL584657 28 bp mRNA linear EST 28-FEB-2001 AL584657 Stratagene Chick Embryo Lambda cDNA Library (* 937405) Gallus gallus cDNA clone ROS012G12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                          Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 28)
Murray, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stratagene Chick Embryo Lambda cDNA Library
Unpublished (2001)
Contact: Frazer Murray
  Pred. No. 5.9e+06;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 18; DB 9; Lo
100.0%; Pred. No. 7.8e+06;
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS012G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dept. Genomics and Bloinformatics
Roslin Institute
Roslin, Mudlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                719 GCTCAAACCTGGGGGCCTGGTACCC 743
                                                                                    6 GCTCACGCGTGGGGGCCCGGTACCC 30
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Best Local Similarity 100.
Matches 18; Conservative
                      Conservative
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BH861248/c
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                                     High qality sequence starts: 1 High qality sequence stops: 1 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 89 Std Error: 0.00 Seq primer: M13RP1
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                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: placenta; Vectór: pBluescript SR-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'"
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Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
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//strah.="Cd428.1"
//strah.="Cd428.1"
//clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
//note="Vector: BlueScriptz SR+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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/organism="Homo sapiens"
/db_xref="GDB-491920"
/db_xref="Taxon:9606"
/clone="IRAGE:71023"
/clone="IRAGE:71023"
/clone="IRAGE:71023"
/clone="IRAGE:71023"
/clone="IRAGE:71023"
/lab_host="SOLR_cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19.6; DB 14; Length 28;
Pred. No. 3.4e+06;
0; Mismatches 4; Indels
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920 E. 58th Street, Chicago, IL 60637,
7El: 773 702 4374
Fax: 773 702 3172
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Molecular Genetics and Cell Biology
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  est@watson.wustl.edu
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Tetrahymena thermophila
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3110 CTTCTCTTCCTCCACCTCTT 3129
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plasmid ends
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                  S. Alonso, J. M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Laimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
L. Ontert. Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Columbia 0"
/db_xref="taxon:3702"
/clone="Salk_067873"
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/clone="pcR was performed on Arabidopsis thaliana lines each of Which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Dunn, D., Aoyad, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                        This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5940020. Class: TDNA tagged.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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80.0%; Pred. No. 1.3e+07;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with THE DNA polymerase and THE polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114) gb[R129072.1], a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacres,S., Mahmoud,M., Meenen,E., Pedersen,T., Really
iM., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhassern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XLI0-Gold, Ti-resistant,
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
lnsert Length: 10000 Std Error: 0.00
Plate: 0017 row: H column: 04
Seq primer: CGTFGTAAAACGACGCCAGT
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                     /organism-"Mus musculus"
High quality sequence stop: 26.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='InAGE:1586115"
/clone=Lib="NoI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/tab_host="hill08"
/note="vector: pr73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to oligo(dT) primer. Double-stranded cDNA was ligated to coligo (dT) primer. Boulde-stranded cDNA was ligated to vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo."
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Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel (A. and Ributcher, L. and Klobutcher, L. and Ributcher, L. Groma Terrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels

    .30 /
/organism="Tetrahymena thermophila"
/strain="CU428.1"

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75.0%; Pred. No. 1.5e+07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

0.4%; Score 16.8; DB 9;
Best Local Similarity 75.0%; Pred. No. 1.5e+07;
Matches 21; Conservative 0; Mismatches 7;
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: apturkew@midway.uchicago.edu
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3164 AGCTGCTCCAAAGACATCCAGTATCTCA 3191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                715 CTCGGCTCAAACCTGGGGGCCTGGTACC 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 ACCTCCTACATTGACATCCAGGACCTCA 1
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Best Local Similarity 75.09
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 773 702 4374
Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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BM398517
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                                                                                                                                                                                                                                                                                                                                                                    (http://www.lax.orgyresources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerlectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 (pb LA29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 23-JUL-1998
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                          /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA973948 23-JUL-1. oq12d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1586115 3' similar to TR:035787 035787 KINESIN-RELATED PROTEIN. ;, mRNA
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                            /sex="Male"
/lab_host="E. Coli strain Xil0-Gold, Tl-resistant, F-"
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                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MOGC2M0017H04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 16.8; DB 17; Length 26; 90.0%; Pred. No. 1.4e+07; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                            /organism="Mus musculus"
     Class: plasmid ends
High quality sequence stop: 26.
                                                         Location/Qualifiers
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AA973948.1 GI:3149128
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 18; Conserv
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DEFINITION

RESULT 9 AZ404206

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ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

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/Jab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymicleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114) pilAR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                   AZ789420 2M0037J11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0037J11 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus Bukaryota; Chordata; Craniata; Vertebrata; Euteleostoml; Bukaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musli (bases 1 to 29)

1 (bases 1 to 29)

10 (bases 1 to 29)

11 (bases 1 to 29)

12 (bases 1 to 29)

13 (bases 1 to 29)

14 (bases 2 to 29)

15 (bases 2 to 29)

16 (bases 3 to 29)

17 (bases 3 to 29)

18 (bases 3 to 29)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Welss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: J column: 11
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
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      1 CTGCTGCTGCTGCTGCTGCT 23
                                                                                                                                                                                                                                                                                                AZ789420.1 GI:12930223
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/lab.host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purplied and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114 glp.HR29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota is Lebraia Rodentia; Sciurognathi; Muridae; Murinae; Mus. E I (bases 1 to 27)

E I (bases 1 to 27)

S Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (200)

L Context: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
Wm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                         A2404206 27 bp DNA linear GSS 03-OCT-2000 lM0172120F Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGClM0172120 F, DNA sequence.
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/organism="Mus musculus"
/strain="C57BL/63"
/strain="Laxon:10090"
/clone="UGGCIM0172120"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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82.6%; Pred. No. 1.6e+07;
tive 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0172 row: I column: 20
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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3 CTGAGCTCACGCGGGGGGCCCGGTACC 30
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                                                                                                                                                                                                                                                                                      AZ404206.1 GI:10528219
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Fax: 801 585 7177
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Matches 19; Conserva
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Gaps ö

Query Match

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BASE COUNT

ORIGIN

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1...22
/organism="Homo sapiens"
/organism="Homo sapiens"
/do_xref="taxon:9606"
/clone="IMAGE:1563821"
/clone="Lib="Soares_NFL_T_GBC_S1"
/lab_bost="bl108"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. Clones 297480-302087, 682632-687239, 726408-728711, and 722096-313399. Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 bp mRNA linear EST 17-JAN-2002 5009-00-41-A08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM398127 GI:18198180
EST.
                                                                                                                                      EST 23-JUN-1998
                                                                                                                                      AA953755 23-JUN-199
on89b03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1563821 3' similar to TR:Q92759 Q92759 TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tunor Gene Index (1997)

Upublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality

Insert Length: 655 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers
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Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 30)
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  4 CACACTGCCAGTTCTTGTACAGGTGC 29
                                                                                                                                                                                                                   AA953755
AA953755 GI:3116673
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Best Local Similarity 85.77
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84.12, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                   A2840149 30 bp DNA linear GSS 20-FEB-2001 2M0136M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0136M06 R, DNA sequence.
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/db_xrsf="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0136 row: M column: 06
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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26 AGTITAAGGATGCAGTCCATCAGAGC
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Class: plasmid ends
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Mus musculus
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                     /organism-"Tetrahymena thermophila"
//strain-"cU428.1"
/db_xref-"taxon:5911
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/clone_lib-"tchilcoat/Turkewitz SK+; Details on library
preparation can be found in chilcoat and Turkewitz (2001)
proc. Natl. Acad. Sci USA, 98: 8709-8713."
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel, J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
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/db_xref="taxon:10090"
/clone="lib="whouse 10kb plasmid UUGClM library"
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                                                                                                                                                   USA
                                                                                 Contact: Turkewitz AP
Molecular Genetics and Cell Biology
Molecular Genetics and Cell Biology
Molecular Genetics and Cell Biology
Molecular Genetics
920 E. 58th Street, Chicago, IL 60637,
Tel: 773 702 4374
Fas: 773 702 3172
Email: apturkew@midway.uchicago.edu
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Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Context: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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AZ343274.1 GI:10421180
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Mus musculus
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84112, USA
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(http://www.jax.orgyresources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) jplART29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.Gold (Stratagene) cells and selected for amplicillin resistance."
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/sex="Male"
//lab_lost="E. Coli strain XL10-Gold, T1-resistant, F-"
//note="Vector: PWH42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 16.2; DB 17; Length 30; 72.4%; Pred. No. 2e+07; tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0420 row: P column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1088 AAACCGCGTGCCAAACCACCTCCCATTCC 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 30.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 AACCCAGGTGCCATACCAGCACTCATACC
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//Ab_host="E. Colid Coli
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Search completed: March 4, 2003, 06:25:19 Job time : 4732 secs